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Sequence Listing could not be accepted.

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Reviewer: Anne Corrigan

Timestamp: Wed Oct 10 10:48:32 EDT 2007

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Reviewer Comments:

<110> APPLICANT: Brockhaus, et al.

<120> TITLE OF INVENTION: Human TNF Receptor

<130> FILE REFERENCE: 01017/40451C

<140> CURRENT APPLICATION NUMBER: US/08/444,790A

<141> CURRENT FILING DATE: 1995-05-19

<150> PRIOR APPLICATION NUMBER: CH 3319/89

<151> PRIOR FILING DATE: 1989-09-12

The above is a sample of global errors: please do not include the alphabetical headings next to the numeric identifiers: just use the numeric identifiers and their responses (e.g., <110> Brockhaus, et al.). Also, please remove the "A" at the end of the <140> response (should just be US/08/444,790).

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Validated By CRFValidator v 1.0.3

Application No: 08444790 Version No: 1.0

Input Set:

Output Set:

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Finished: 2007-09-20 18:09:45.706
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Total Errors: 0
No. of SeqIDs Defined: 26
Actual SeqID Count: 26

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Input Set:

Output Set:

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This error has occured more than 20 times, will not be displayed

<110> APPLICANT: Brockhaus, et al.
<120> TITLE OF INVENTION: Human TNF Receptor
<130> FILE REFERENCE: 01017/40451C
<140> CURRENT APPLICATION NUMBER: US/08/444,790A
<141> CURRENT FILING DATE: 1995-05-19
<150> PRIOR APPLICATION NUMBER: CH 3319/89
<151> PRIOR FILING DATE: 1989-09-12
<150> PRIOR APPLICATION NUMBER: CH 786/90
<151> PRIOR FILING DATE: 1990-03-08
<150> PRIOR APPLICATION NUMBER: CH 1347/90
<151> PRIOR FILING DATE: 1990-04-20
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<150> PRIOR APPLICATION NUMBER: US 08/095,640
<151> PRIOR FILING DATE: 1993-07-21
<160> NUMBER OF SEQ ID NOS: 26
<170> SOFTWARE: PatentIn version 3.3

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<211> LENGTH: 2111
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 1

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ccagcactgc cgctgccaca ctgccctgag cccaaatggg ggagtgagag gccatagctg 180
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aagagagata gtgtgtgtcc ccaaggaaaa tatatccacc ctcaaaataa ttcgatttgc 360
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gttttgtttt taaatcaatc atgttacact aatagaaact tggcactcct gtgccctctg 1980
cctggacaag cacatagcaa gctgaactgt cctaaggcag gggcgagcac ggaacaatgg 2040

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aacccgaatt c 2111

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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 2

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His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
35 40 45
Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
50 55 60
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
65 70 75 80
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
85 90 95
Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
100 105 110
Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
115 120 125
Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
130 135 140
Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
145 150 155 160
Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
165 170 175
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
180 185 190
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
195 200 205
Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
210 215 220
Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
225 230 235 240
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
245 250 255
Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
260 265 270
Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
275 280 285
Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
290 295 300
Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
305 310 315 320
Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
325 330 335
Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
340 345 350
Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
355 360 365
Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
370 375 380
Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln

```
385                 390                 395                 400
Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
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Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
            420                 425                 430
Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
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Pro Ala Pro Ser Leu Leu Arg
    450                 455
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<211> LENGTH: 2339
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 3

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caggaggggt gccggctgtg cgcgccgctg ccgaagtgcc gcccgggctt cggcgtggcc    240
agaccaggaa ctgaaacatc agacgtggtg tgcaagccct gtgccccggg gacgttctcc    300
aacacgactt catccacgga tatttgcagg ccccaccaga tctgtaacgt ggtggccatc    360
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ccaggggcag tacacttacc ccagccagtg tccacacgat cccaacacac gcagccaagt    480
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gctgaaggga gcactggcga cttcgctctt ccagttggac tgattgtggg tgtgacagcc    600
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ccaggcgtgg aggccagtgg ggccggggag gcccgggcca gcaccgggag ctcagcagat    900
tcttcccctg gtggccatgg gacccaggtc aatgtcacct gcatcgtgaa cgtctgtagc    960
agctctgacc acagctcaca gtgctcctcc caagccagct ccacaatggg agacacagat   1020
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tttaaaaaag taagtaccac tcaggccaac aagccaacga caaagccaaa ctctgccagc   2280
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<212> TYPE: PRT
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Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
        35                  40                  45
Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
    50                  55                  60
Arg Leu Cys Ala Pro Leu Pro Lys Cys Arg Pro Gly Phe Gly Val Ala
65                  70                  75                  80
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
                85                  90                  95
Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
            100                 105                 110
Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala
        115                 120                 125
Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
    130                 135                 140
His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Ser
145                 150                 155                 160
Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
                165                 170                 175
Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val
            180                 185                 190
Gly Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val
        195                 200                 205
Val Asn Cys Val Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu
    210                 215                 220
Gln Arg Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala Arg Gly
225                 230                 235                 240
Thr Gln Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser
                245                 250                 255
Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala
            260                 265                 270
Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala
        275                 280                 285
Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Ala Asp Ser Ser Pro Gly
    290                 295                 300
Gly His Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser
305                 310                 315                 320
Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met
                325                 330                 335
Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val
            340                 345                 350
Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro
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<212> TYPE: PRT

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<223> OTHER INFORMATION: Synthetic peptide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (25)..(25)
<223> OTHER INFORMATION: Xaa = any or unknown amino acid
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Gln Gly Lys Tyr Ile His Pro Glu Xaa Asn Ser Ile
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1 5 10 15
Pro Leu

<210> SEQ ID NO 8
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<210> SEQ ID NO 9
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1 5 10 15

<210> SEQ ID NO 10
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<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Xaa = any or unknown amino acid
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Thr Cys

<210> SEQ ID NO 11
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<212> TYPE: PRT
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<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: Xaa = any or unknown amino acid
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<210> SEQ ID NO 12
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<210> SEQ ID NO 13
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<212> TYPE: PRT
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<223> OTHER INFORMATION: Synthetic peptide
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<210> SEQ ID NO 14
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<223> OTHER INFORMATION: Xaa = any or unknown amino acid
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<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: Xaa = any or unknown amino acid
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1 5 10 15

<210> SEQ ID NO 15
<211> LENGTH: 9
<212> TYPE: PRT
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1 5

<210> SEQ ID NO 16
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic primer
<400> SEQUENCE: 16
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<210> SEQ ID NO 17
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Synthetic primer
<400> SEQUENCE: 17
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